

Remarks/Arguments

Claim 32 is allowed, claims 2 and 34 are objected to and claims 1, 4-8, 10, 11 and 13-15 are rejected. New claim 35 has been added. Claims 1, 4-8, 10-11, 13-15, 32 and 35 are pending. In the present response, claim 1 has been amended, claims 2 and 34 have been canceled without prejudice or disclaimer and new claim 35 has been added. Support for amended claim 1 can be found in the previously presented claims 2 and 34. Support for newly added claim 35 can be found in claims 32, 34 and throughout the specification.

Applicants have revised the paragraph beginning on line 22, page 4 of the specification to show that the genbank numbers for human and mouse dab1 are mRNAs instead of genes.

No new matter has been added by way of these amendments to the claims and specification. Reconsideration and withdrawal of the rejections are respectfully requested in light of these amendments and the following remarks.

In paragraph 4 of the Office Action dated February 21, 2006, the Examiner states that Applicants failed to provide an amendment directing entry of the paper copy of the sequence listing into the specification. Applicants respectfully disagree. On page 6 of Applicant's response dated November 21, 2005, the first sentence of the second paragraph states: "In place of the canceled sequence listing, Applicants request that the paper copy of the sequence listing filed herein be entered into the specification." However, to further prosecution, Applicants have provided an amendment to the sequence listing found on page 5 of this response.

Specification/Informalities

The Examiner pointed out that the paragraph beginning on line 22, page 4 of the specification contains new matter. Applicants apologize for this error and have revised this paragraph to replace dab1 "gene" with "mRNA".

35 U.S.C § 112, Second Paragraph

Claims 1, 4-8, 10-11 and 13-15 are rejected under 35 USC 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject

matter which Applicants regards as the invention. The Examiner asserts that the recitation of "a serine corresponding to position 491 of the polypeptide encoded by SEQ ID NO:4 and a serine corresponding to position 515 of the polypeptide encoded by SEQ ID NO:4" as it relates to a Dab1 comprising SEQ ID NO:3 is confusing and asks Applicants to clarify the meaning of the claim. The Examiner asserts that it is unclear as to which serine of a dab1 comprising SEQ ID NO:3 is intended as "corresponding to" position 491 or 515 of the polypeptide encoded by SEQ ID NO:4. The Examiner states that in accordance with MPEP 2111, the Examiner has interpreted the term "a serine corresponding to position 491 of the polypeptide encoded by SEQ ID NO:4 and a serine corresponding to position 515 of the polypeptide encoded by SEQ ID NO:4" as meaning any serine with a Dab1 polypeptide comprising SEQ ID NO:3. The Examiner asks that Applicants clarify the meaning of the term.

Applicants continue to assert that Dab1 proteins can easily be distinguished by a person of skill in the art and that structural references are not needed to identify a Dab1 protein. However, Applicants revised claim 1 so that if a Dab1 protein does not comprise the 14 amino acid sequence of SEQ ID NO:3, then that protein would lie outside the scope of the claim. Attached as Exhibit 1 is a list of proteins that contain conserved domains when compared to the Dab1 protein encoded by genbank no. 1771282 (SEQ ID NO:4). The first 17 proteins listed are either described as "Dab1 proteins" or "predicted: similar to Dab1 proteins". Furthermore, all of the first 16 proteins listed contain SEQ ID NO:3. Dab1 from *Danio rerio*, gi68440873, (number 17 on the list) is the first Dab1 protein listed that does not contain this 14 amino acid sequence, and it differs only in 1 amino acid (see Exhibit 6). Furthermore, other proteins listed such as mDab271, unnamed protein, Chain B, disabled homolog 2 isoform b, etc. do not share homology with SEQ ID NO:3.

While serine 491 of SEQ ID NO:4 falls within SEQ ID NO:3, serine 515 does not. Inclusion of SEQ ID NO:3 in the claim is independent of the positioning of "a serine corresponding to position 491 or 515 of SEQ ID NO:4". SEQ ID NO:3 was added to the claim to provide a structural reference to distinguish it from other materials.

Applicants provide as Exhibits 2 - 6 alignments of Homo sapiens, Canis familiaris, Gallus gallus, Bos taurus and Danio rerio Dab1 proteins with the Mus musculus Dab1 protein. Applicants show that a person of skill in the art using this amino acid sequence alignment can easily identify a serine from the Dab1 protein of any species that corresponds to serine 491 or 515 of murine Dab1.

However, in an attempt to further prosecution, Applicants have amended claim 1 to state that a phosphorylated serine at position 491 or 515 of SEQ ID NO:4 or SEQ ID NO:5 is indicative of Cdk5 serine kinase activity.

In view of the above arguments and amendments, all grounds for the rejection under 35 U.S.C. § 112, second paragraph have been obviated or overcome. Reconsideration and withdrawal of this rejection are respectfully requested.

35 U.S.C. § 112, First Paragraph

The Examiner rejected claims 1, 4-8, 10-11 and 13-15 under 35 USC 112, first paragraph, for failing to comply with the written description requirement. The Examiner rejected the claims for introducing new matter based on the addition of SEQ ID NO:3. The Examiner also maintained the previous scope of enablement rejection of Claims 1, 4-8, 10-11 and 13-15. The Examiner asserts that the claims are drawn to a method for detecting Cdk5 activity by determining whether a genus of Dab1 proteins is phosphorylated on a specific serine and that an invention involving a genus requires a precise definition, such as a structure, formula or chemical name of the claimed subject matter to sufficiently distinguish it from other materials.

Applicants disagree. SEQ ID NO: 3 is provided as a structural reference for the genus of Dab1 protein. A peptide having the sequence of SEQ ID NO:3 as shown in the specification was used as an antigen to generate an antibody that binds to Dab1. The use of this peptide as an antigen as described in the specification reveals to one of skill in the art that this is a sequence useful for distinguishing Dab1 from other proteins. Therefore, it is entirely appropriate for Applicants to use SEQ ID NO:3 in the claims for this purpose. Doing so does not introduce new matter into the specification.

However, in an effort to further prosecution, Applicants have amended Claim 1 to recite a serine phosphorylated at position 491 or 515 of SEQ ID NO:4 or SEQ ID NO:5 is

indicative of Cdk5 serine kinase activity. Reference to SEQ ID NO:3 has been removed, rendering the new matter rejection moot.

Amendment of Claim 1 to recite a particular serine of SEQ ID NO:4 or SEQ ID NO:5 focuses the scope of the claims to that which is enabled by the teachings of the specification.

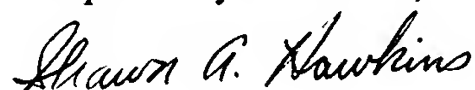
In view of the above arguments and amendments, all grounds for the rejections under 35 U.S.C. § 112, first paragraph have been obviated or overcome. Reconsideration and withdrawal of these rejections are respectfully requested.

Conclusion


It is believed that all the rejections have been obviated or overcome and the claims are in condition for allowance.

It is not believed that extensions of time or fees for net addition of claims are required. However, in the event that additional extensions of time are necessary to allow consideration of this paper, such extensions are hereby petitioned under 37 CFR § 1.136(a), and any fee required therefore (including fees for net addition of claims) is hereby authorized to be charged to Deposit Account No. 501968.

Respectfully submitted,



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Registration No. 50,318

	BLAST	Protein	Structure	PubMed	Taxonomy
	Genome	Nucleotide	3D-Domains	Books	Help

Query: gi|1771282 mDab555 protein [Mus musculus]

Matching gi: 70909361

[Show identical](#)[Best hits](#)[Common Tree](#)[Taxonomy Report](#)[3D structures](#)[CDD-Search](#)[G](#)

199 BLAST hits to 23 unique species Sort by taxonomy proximity

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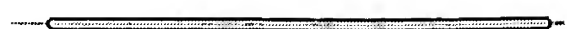


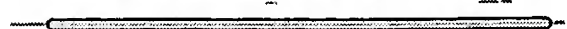
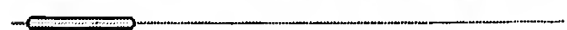

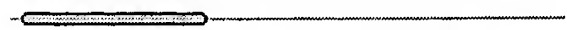





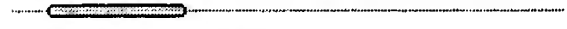
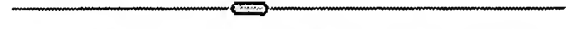
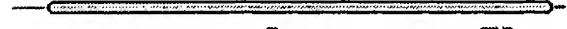

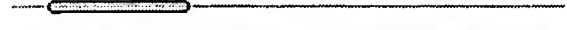

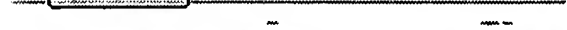



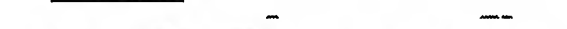
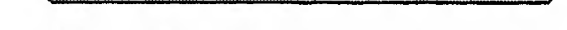





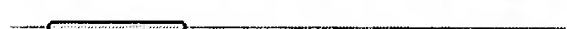


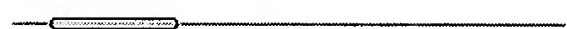
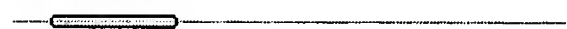



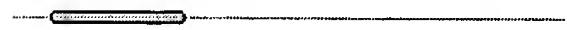
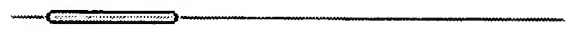
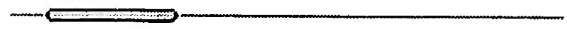
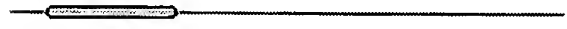

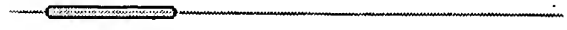
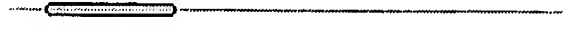
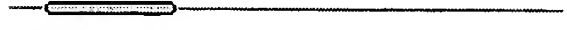
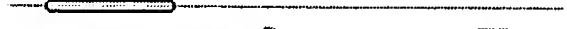
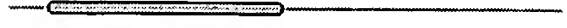

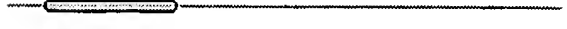
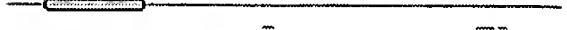

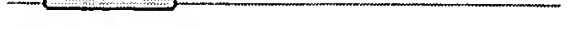
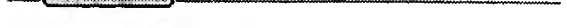




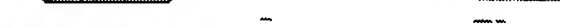




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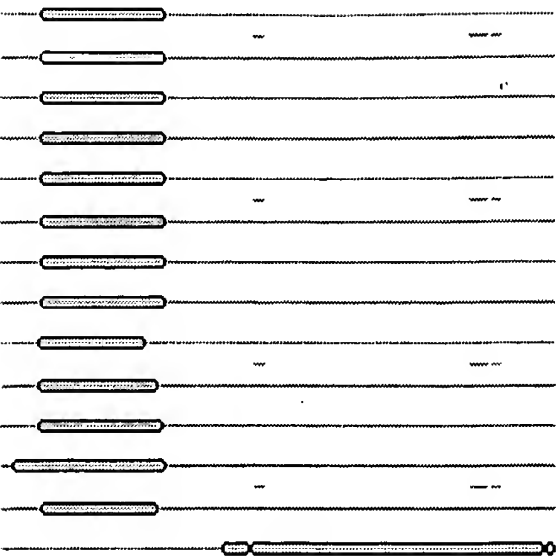
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555 aa

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2	2844	30	P97318	20137771	Disabled homolog 1
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4	2805	22	CAI22361	56205777	disabled homolog 1 (Drosophila) [Homo sap
5	2797	22	O75553	20137706	Disabled homolog 1
6	2791	22	Q9BGX5	20137926	Disabled homolog 1
7	2766	22	AAF73058	8118615	disabled-1 [Homo sapiens]
8	2761	22	CAI22362	56205778	disabled homolog 1 (Drosophila) [Homo sap
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11	2605	18	NP_989569	45383654	disabled homolog 1 [Gallus gallus]
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14	2424	21	XP_582976	76613795	PREDICTED: similar to Disabled homolog 1
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	154	22	NP_001...	54144627	numb homolog isoform 2 [Homo sapiens]
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	153	28	ABC69735	85070124	numb isoform o/o [Rattus norvegicus]
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	151	22	AAD27959	4691549	NUMB protein [Homo sapiens]
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	150	21	XP_588484	76611402	PREDICTED: similar to low density lipoprotein
	150	28	XP_220798	62656707	PREDICTED: similar to ubiquitin specific
	150	30	AAH33459	23270973	Numb protein [Mus musculus]
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	148	28	ABC69734	85070122	numb isoform i/o [Rattus norvegicus]
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	147	30	NP_035079	6754912	numb gene homolog [Mus musculus]
	147	30	BAE35380	74204621	unnamed protein product [Mus musculus]
	147	30	Q8C142	73921719	Low density lipoprotein receptor adapter
	147	28	XP_575931	62649833	PREDICTED: similar to LDL receptor adaptor
	147	21	XP_867847	73963533	PREDICTED: similar to numb homolog isoform
	147	30	BAC26238	26324968	unnamed protein product [Mus musculus]
	146	17	CAJ81873	89273752	OTTXETP00000000331 [Xenopus tropicalis]
	146	18	XP_417736	50759690	PREDICTED: similar to LDL receptor adaptor
	145	17	Q67FQ3	73921717	Low density lipoprotein receptor adapter
	145	17	AAH68810	46250128	MGC81404 protein [Xenopus laevis]
	145	21	XP_867889	73963545	PREDICTED: similar to numb homolog isoform
	145	21	XP_855049	73950589	PREDICTED: similar to low density lipoprotein
	145	17	Q801G1	73921716	Low density lipoprotein receptor adapter
	143	15	XP_695452	68438641	PREDICTED: similar to GULP, engulfment ad
	141	21	XP_885051	76641663	PREDICTED: similar to numb homolog (Droso
	141	21	XP_885074	76641665	PREDICTED: similar to numb homolog (Droso
	139	7	CAE64299	39584875	Hypothetical protein CBG08974 [Caenorhabd
	138	22	BAB14908	10436776	unnamed protein product [Homo sapiens]
	138	22	AAH29770	20987600	ARH protein [Homo sapiens]
	138	30	NP_663529	21704092	low density lipoprotein receptor adaptor
	137	22	CAD66588	28375609	unnamed protein product [Homo sapiens]
	137	30	AAD47834	5713183	71 kDa Numb protein isoform [Mus musculus]
	137	21	XP_537504	73963551	PREDICTED: similar to numb homolog isoform
	137	1	AAX36723	60825530	numb-like [synthetic construct]
	137	21	XP_867842	73963531	PREDICTED: similar to numb homolog isoform
	137	21	XP_867882	73963543	PREDICTED: similar to numb homolog isoform
	137	22	AAH20788	18088523	NUMB protein [Homo sapiens]
	137	28	ABC69736	85070126	numb isoform o/i [Rattus norvegicus]
	136	15	AAI07954	79160060	Numb homolog [Danio rerio]
	134	15	BAD89560	59275985	numb homolog [Danio rerio]
	134	15	CAG09924	47219570	unnamed protein product [Tetraodon nigrov
	133	30	1WJ1A	56966911	Chain A, Solution Structure Of Phosphotyros
	133	15	CAI21213	56208059	novel protein containing a phosphotyrosin
	133	15	NP_945331	39752651	hypothetical protein LOC368278 [Danio rer
	132	22	CAD62362	28193240	unnamed protein product [Homo sapiens]
	132	22	XP_510045	55641017	PREDICTED: similar to NUMB protein [Pan t
	132	22	NP_001...	54144625	numb homolog isoform 1 [Homo sapiens]
	132	30	Q9QZS3	14194994	Protein numb homolog (m-Numb) (m-Nb)
	132	21	XP_867897	73963547	PREDICTED: similar to Numb protein homolo
	132	28	ABC69737	85070128	numb isoform i/i [Rattus norvegicus]
	131	7	AAW26009	56755661	SJCHGC02254 protein [Schistosoma japonicu
	131	17	AAI06374	76780336	Unknown (protein for MGC:130936) [Xenopus
	129	30	BAE27971	74184738	unnamed protein product [Mus musculus]



129	28	NP_001...	76559905	numb-like [Rattus norvegicus]
129	1	AAX32221	60655315	numb-like [synthetic construct]
129	21	XP_855314	73948318	PREDICTED: similar to numb homolog (Droso
129	22	Q9Y6R0	14194976	Numb-like protein (Numb-R)
129	30	O08919	51704231	Numb-like protein
129	30	NP_035080	87042277	numb-like [Mus musculus]
129	30	AAB58697	2149943	Numblake [Mus musculus]
128	15	CAG06441	47224871	unnamed protein product [Tetraodon nigrov
128	22	XP_524622	55586633	PREDICTED: hypothetical protein XP_524622
128	15	CAG09113	47224267	unnamed protein product [Tetraodon nigrov
126	8	EAL26939	54637537	GA18153-PA [Drosophila pseudoobscura]
126	7	AAX24514	76152838	SJCHGC02255 protein [Schistosoma japonicu
125	22	CAH91693	55729933	hypothetical protein [Pongo pygmaeus]
124	4	NP_982814	45185097	ABL133Cp [Eremothecium gossypii]



Blast 2 Sequences results

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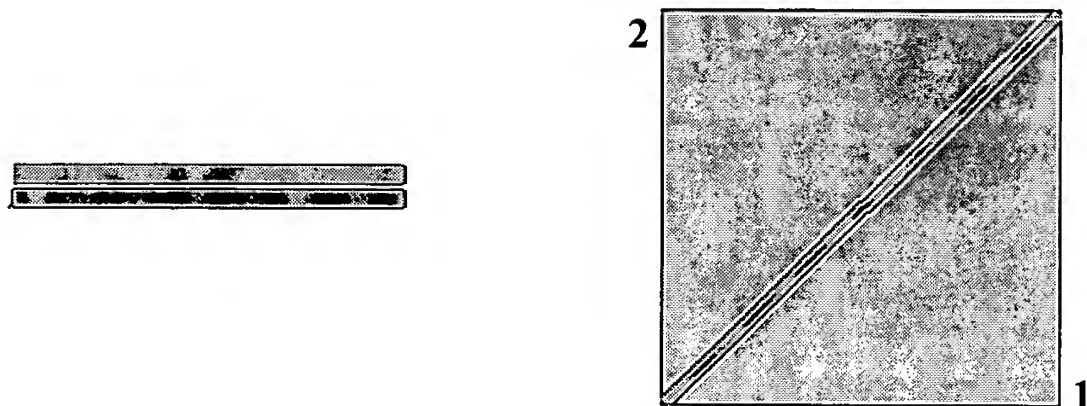
BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.13 [Nov-27-2005]

Matrix **BLOSUM62** gap open: **11** gap extension: **1**x_dropoff: **50** expect: **300.00** wordsize: **3** Filter ☐ View option **Standard**Masking character option **X for protein, n for nucleotide** Masking color option **Black**☐ Show CDS translation **Align****Sequence 1:** gi|1771282|emb|CAA69662.1|mDab555 protein [Mus musculus]

Length = 555 (1 .. 555)

Sequence 2: gi|68533079|dbj|BAE06094.1|DAB1 variant protein [Homo sapiens]

Length = 559 (1 .. 559)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 1085 bits (2805), Expect = 0.0

Identities = 536/555 (96%), Positives = 543/555 (97%), Gaps = 0/555 (0%)

Query	1	MSTETELQVAVKTSAKKDSRKKGQDRSEATLIKRFKGEVRYKAKLIGIDEVSAARGDKL	60
		MSTETELQVAVKTSAKKDSRKKGQDRSEATLIKRFKGEVRYKAKLIGIDEVSAARGDKL	
Sbjct	5	MSTETELQVAVKTSAKKDSRKKGQDRSEATLIKRFKGEVRYKAKLIGIDEVSAARGDKL	64
Query	61	CQDSMMKLKGVVAGARSKGEHKQKIFLTISFGGIKIFDEKTGALQHHHAVHEISYIAKDI	120
		CQDSMMKLKGVVAGARSKGEHKQKIFLTISFGGIKIFDEKTGALQHHHAVHEISYIAKDI	
Sbjct	65	CQDSMMKLKGVVAGARSKGEHKQKIFLTISFGGIKIFDEKTGALQHHHAVHEISYIAKDI	124
Query	121	TDHRAFGYVCGKEGNHRFVAIKTAQAAEPVILDLRDLFQLIYELKQREELEKKAQKDKQC	180
		TDHRAFGYVCGKEGNHRFVAIKTAQAAEPVILDLRDLFQLIYELKQREELEKKAQKDKQC	
Sbjct	125	TDHRAFGYVCGKEGNHRFVAIKTAQAAEPVILDLRDLFQLIYELKQREELEKKAQKDKQC	184
Query	181	EQAVYQTILEEDVEDPVYQYIVFEAGHEPIRDPETEENIYQVPTSQKKEGVYDVPKSQPV	240
		EQAVYQTILEEDVEDPVYQYIVFEAGHEPIRDPETEENIYQVPTSQKKEGVYDVPKSQPV	
Sbjct	185	EQAVYQTILEEDVEDPVYQYIVFEAGHEPIRDPETEENIYQVPTSQKKEGVYDVPKSQPV	244
Query	241	SAVTQLELFGDMSTPPDITSPPTPATPGDAFLPSSSQTLPGSADVFGSMSFGTAAVPSGY	300
		SAVTQLELFGDMSTPPDITSPPTPATPGDAF+PSSSQTLP SADVF S+ FGTAAVPSGY	

Blast Result

Sbjct 245 SAVTQLELEFGDMSTPPDITSPPTPATPGDAFIPSSSQTLPASADVFSVPFGTAAVPSGY 304

Query 301 VAMGAVLPSFWGQQPLVQQQIAMGAQPPVAQVIPGAQPIAWGQPGLFPATQQAWPTVAGQ 360
VAMGAVLPSFWGQQPLVQQQ+ MGAQPPVAQV+PGAQPIAWGQPGLFPATQQ WPTVAGQ

Sbjct 305 VAMGAVLPSFWGQQPLVQQQMVMGAQPPVAQVMPGAQPIAWGQPGLFPATQQPWPTVAGQ 364

Query 361 FPPAAFMPTQTVMPLAAAMFQGPLTPLATVPGTND SARSSPQSDKPRQKMGKESFKDFQM 420
FPPAAFMPTQTVMPL AAMFQGPLTPLATVPGT+DS RSSPQ+DKPRQKMGKE+FKDFQM

Sbjct 365 FPPAAFMPTQTVMPLPAAMFQGPLTPLATVPGTSDSTRSSPQTDKPRQKMGKETFKDFQM 424

Query 421 VQPPPVP SRKPDQPSLTCTSEAFSSYFNKVGVAQDTDDCDDFDISQLNLTPVTSTTPSTN 480
QPPPVP SRKPDQPSLTCTSEAFSSYFNKVGVAQDTDDCDDFDISQLNLTPVTSTTPSTN

Sbjct 425 AQPPPVP SRKPDQPSLTCTSEAFSSYFNKVGVAQDTDDCDDFDISQLNLTPVTSTTPSTN 484

Query 481 SPPTPAPRQSSPSKSSASHVSDPTADDIFEEGFESPSKSEEQEAPDGSQASSTSDPFGE 540
SPPTPAPRQSSPSKSSASH SDPT DDIFEEGFESPSKSEEQEAPDGSQASS SDPFGE

Sbjct 485 SPPTPAPRQSSPSKSSASHASDPTTDDIFEEGFESPSKSEEQEAPDGSQASSNSDPFGE 544
1-56010 NO:3 -1

Query 541 SGEPSGDNISPQDGS 555
SGEPSGDNISPQ GS

Sbjct 545 SGEPSGDNISPQAGS 559

CPU time: 0.05 user secs. 0.02 sys. secs 0.07 total secs.

Lambda K H
0.311 0.129 0.373

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 3330

Number of extensions: 1692

Number of successful extensions: 10

Number of sequences better than 300.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 555

Length of database: 1,196,146,007

Length adjustment: 138

Effective length of query: 417

Effective length of database: 1,196,145,869

Effective search space: 498792827373

Effective search space used: 498792827373

Neighboring words threshold: 9

X1: 16 (7.2 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 42 (21.8 bits)

S2: 68 (30.8 bits)



Blast 2 Sequences results

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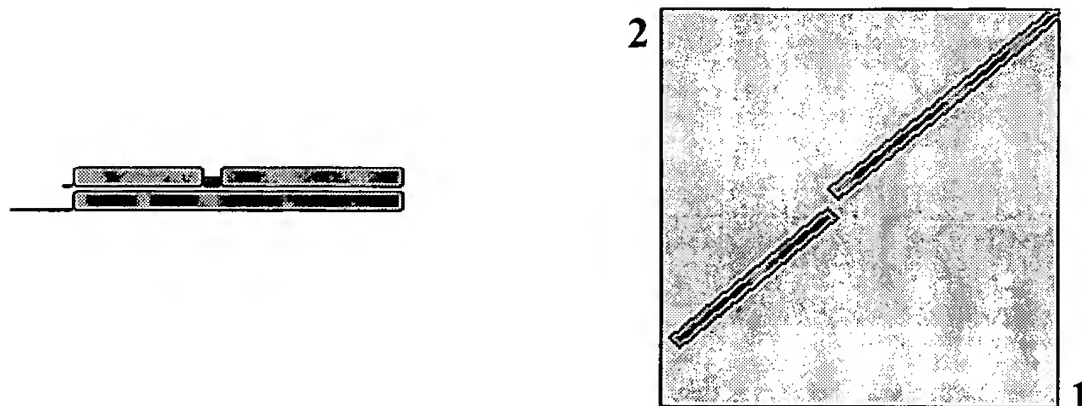
BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.13 [Nov-27-2005]

Matrix gap open: gap extension: x_dropoff: expect: wordsize: Filter ☐ View option Masking character option Masking color option ☐ Show CDS translation **Sequence 1:** gi|1771282|emb|CAA69662.1|mDab555 protein [Mus musculus]

Length = 555 (1 .. 555)

Sequence 2: gi|73956392|ref|XP_852920.1|PREDICTED: similar to Disabled homolog 1 [Canis familiaris]

Length = 678 (1 .. 678)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 1024 bits (2648), Expect = 0.0

Identities = 513/567 (90%), Positives = 520/567 (91%), Gaps = 33/567 (5%)

Query	22	KGQDRSEATLIKRFKGEVRYKAKLIGIDEVSAARGDKLCQDSMMKLKGVVAGARSKGEH	81
		+GQDRSEATLIKRFKGEVRYKAKLIGIDEVSAARGDKLCQDSMMKLKGVVAGARSKGEH	
Sbjct	112	QGQDRSEATLIKRFKGEVRYKAKLIGIDEVSAARGDKLCQDSMMKLKGVVAGARSKGEH	171
Query	82	KQKIFLTISFGGIKIFDEKTGALQHHHAVHEISYIAKDITDHRAFGYVCGKEGNHRFVAI	141
		KQKIFLTISFGGIKIFDEKTGALQHHHAVHEISYIAKDITDHRAFGYVCGKEGNHRFVAI	
Sbjct	172	KQKIFLTISFGGIKIFDEKTGALQHHHAVHEISYIAKDITDHRAFGYVCGKEGNHRFVAI	231
Query	142	KTAQAAEPVILDLRDLFQLIYELKQREELEKKAQKDKQCEQAVYQTILEEDVEDPVYQYI	201
		KTAQAAEPVILDLRDLFQLIYELKQREELEKKAQKDKQCEQAVYQTILEEDVEDPVYQYI	
Sbjct	232	KTAQAAEPVILDLRDLFQLIYELKQREELEKKAQKDKQCEQAVYQTILEEDVEDPVYQYI	291
Query	202	VFEAGHEPIRDPETEENIYQVPTSQKKEGVYDVPKSQPVS-----	241
		VFEAGHEPIRDPETEENIYQVPTSQKKEGVYDVPKSQPVS	
Sbjct	292	VFEAGHEPIRDPETEENIYQVPTSQKKEGVYDVPKSQPVSNQPFEDFEERFAAATPNRN	351
Query	242	-----AVTQLELFGDMSTPPDITSPPTPATPGDAFLPSSSQTLPGSADVFGS	288
		AVTQLELFGDMSTPPDITSPPTPATPGDAF+PSSSQTLP SAD+F S	

Blast Result

```
Sbjct 352 LPMDFDEILEATKAVTQLELFGDMSTPPDITSPPTPATPGDAFIPSSSQTLPASADMESS 411

Query 289 MSFGTAAVPSGYVAMGAVLPSFWGQQPLVQQQIAMGAQPPVAQVIPGAQPIAWGQPGLFP 348
+ FGTAAVPSGYVAMGAVLPSFWGQQPLVQQQIAMGAQPPVAQV+PGAQPIAWGQPGLFP
Sbjct 412 VPFGTAAVPSGYVAMGAVLPSFWGQQPLVQQQIAMGAQPPVAQVMPGAQPIAWGQPGLFP 471

Query 349 ATQQAWPTVAGQFPPAAFMPTQTVMPLAAAMFQGPLTPLATVPGTND SARSSPQSDKPRQ 408
ATQQ WPTVAGQFPPAAFMPTQTVMPL AAMFQGPLTPLATVP T DS RSSPQ++KPRQ
Sbjct 472 ATQQPWPTVAGQFPPAAFMPTQTVMPLPAAMFQGPLTPLATVPTTGDSTRSSPQTEKPRQ 531

Query 409 KMGKESFKDFQMVQPPPVPSRKPDQPSLTCTSEAFSSYFNKVGVAQDTDDCDDFDISQLN 468
KMGKE FKDFQM QPPPVPSRKPDQPSLTCTSEAFSSYFNKVGVAQDTDDCDDFDISQLN
Sbjct 532 KMGKEMFKDFQMAQPPPVPSRKPDQPSLTCTSEAFSSYFNKVGVAQDTDDCDDFDISQLN 591

Query 469 LTPVTSTTPSTNSPPTPAPROSSPSKSSASHVSDPTADDIFEEGFESPSKSEEQEAPDGS 528
LTPVTSTTPSTNSPPTPAPROSSPSKSSASH SDPT DDIFEEGFESPSKSEEQEAPDGS
Sbjct 592 LTPVTSTTPSTNSPPTPAPROSSPSKSSASHASDPTTDDIFEEGFESPSKSEEQEAPDGS 651

Query 529 QASSTSDPFGEPSGEPGSGDNISPQDGS 555
QASS SDPFGEPSGEPGSGDNISPQ GS
Sbjct 652 QASSNSDPFGEPSGEPGSGDNISPQAGS 678
```

CPU time: 0.05 user secs. 0.01 sys. secs 0.06 total secs.

Lambda K H
0.311 0.129 0.373

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 3685

Number of extensions: 1958

Number of successful extensions: 11

Number of sequences better than 300.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 555

Length of database: 1,196,146,007

Length adjustment: 138

Effective length of query: 417

Effective length of database: 1,196,145,869

Effective search space: 498792827373

Effective search space used: 498792827373

Neighboring words threshold: 9

X1: 16 (7.2 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 42 (21.8 bits)

S2: 68 (30.8 bits)



Blast 2 Sequences results

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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.13 [Nov-27-2005]

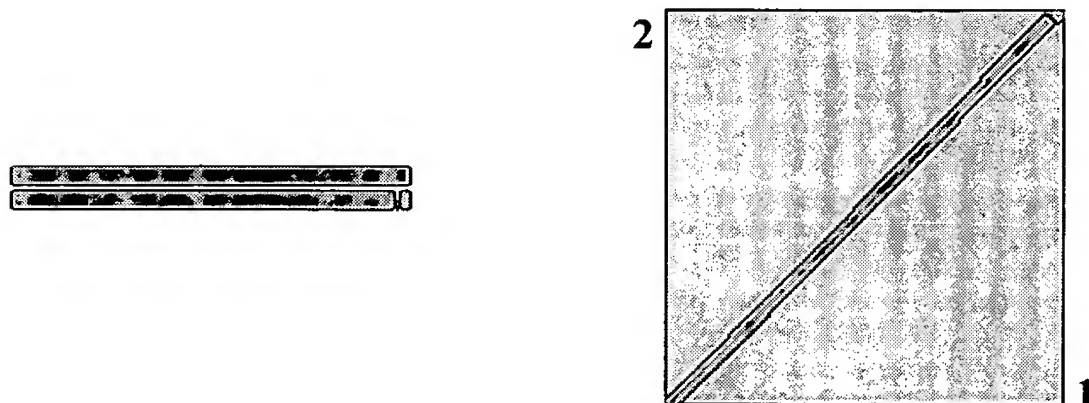
Matrix gap open: gap extension:
x_dropoff: expect: wordsize: Filter ☐ View option
Masking character option Masking color option
☐ Show CDS translation

Sequence 1: gi|1771282|emb|CAA69662.1|mDab555 protein [Mus musculus]

Length = 555 (1 .. 555)

Sequence 2: gi|37933763|gb|AAP70754.1|disabled-1 late isoform [Gallus gallus]

Length = 551 (1 .. 551)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.



Score = 1013 bits (2620), Expect = 0.0

Identities = 497/555 (89%), Positives = 523/555 (94%), Gaps = 4/555 (0%)

Query	1	MSTETELQVAVKTS AKKDSRKKGQDRSEATLIKRFKGEGVRYKAKLIGIDEVSAARGDKL	60
Sbjct	1	MSTETELQVAVKTS KKDS+KKGQDRSEATLIKRFKG+GVRYKAKLIGIDEVSAARGDKL	60
Query	61	CQDSMMKLKGVVAGARSKGEHKQKIFLTISFGGIKIFDEKTGALQH HHAVHEISYIAKDI	120
Sbjct	61	CQDSMMKLKG+VA ARSKGEHKQKIFLT+SFGGIKIFDEKTG LQH HHAVHEISYIAKDI	120
Query	121	TDHRAFGYVCGKEGNHRFVAIKTAQAAEPVILDLRDLFQLIYELKQREELEKKAQKDKQC	180
Sbjct	121	TDHRAFGYVCGKEGNHRFVAIKTAQAAEPVILDLRDLFQLIYELKQREE+EKKAQKDKQC	180
Query	181	EQAVYQTILEEDVEDPVYQYIVFEAGHEPIRDPETEENIYQVPTSQKKEGVYDVPKSQPV	240
Sbjct	181	EQAVYQTILEEDVEDPVYQYIVFEAGHEPIREPETEENIYQVPTSQKKEGVYDVPKSQPV	240
Query	241	SAVTQLELFGDMSTPPDITSPPTPATPGDAFLPSSSQTLPGSADVFGSMSFGTAAVPSGY	300
Sbjct	241	SAVTQLELFGDMSTPPD+TSPPTPATPGDAF+PSSSQ+LP S D+FGS+ F TAAVPSGY	300

Blast Result

Sbjct 241 SAVTQLELEFGDMSTPPDVTSPPTPATPGDAFIPSSSQSLPASTDMFGSVPFESTA AVPSGY 300

Query 301 VAMGAVLPSFWGQQPLVQQQIAMGAQPPVAQVIPGAQPIAWGQPGLFPATQQAWPTVAGQ 360
VAMGAVLPSFWGQQPLVQQQ+AMGAQPPVAQV+ G QPIAWGQPG+FP QQ WP+VAGQ

Sbjct 301 VAMGAVLPSFWGQQPLVQQQLAMGAQPPVAQVMQGGQPIAWGQPGIFPPAQQPWPSVAGQ 360

Query 361 FPPAAFMTQTVMPLAAAMFQGPLTPLATVPGTND SARSSPQSDKPRQKMGKESFKDFQM 420
F P AFMTQT TV+PL AAMFQG + P+ATVP T+DS RSSPQ+D+PRQKMGKE FKDFQM

Sbjct 361 FQPTAFMTQT TVLPLQAAMFQGTI APIATVPPTS DSNRSSPQTDRPRQKMGKEMFKDFQM 420

Query 421 VQPPPVPSRKPDQPSLTCTSEAFSSYFNKVGVAQDTDDCDDFDISQLNLTPVTSTTPSTN 480
QPPPVPSRKPDQPSL+CTSEAFSSYFNKVG+AQ+ DDCDDFDISQLNLTPVTSTTPSTN

Sbjct 421 AQPPPVPSRKPDQPSLSCTSEAFSSYFNKVGMAQEADDCDDFDISQLNLTPVTSTTPSTN 480

Query 481 SPPTPAPROSSPSKSSASHVSDPTADDIFE EGFESPSKSEEQEAPDGSQASSTSDPFGE P 540
SPPTPAPROSSPSKSSASH SDP ADD+FE EGFESPSKSEEQEAPD SQASS SDPF

Sbjct 481 SPPTPAPROSSPSKSSASHTSDPAADDLFE EGFESPSKSEEQEAPDESQASSNSDPF--- 537
1- SEPTDND:3-1

Query 541 SGEPSGDNISPQDGS 555
GEP+GD ISPQ GS

Sbjct 538 -GEPTGDTISPQVGS 551

CPU time: 0.05 user secs. 0.01 sys. secs 0.06 total secs.

Lambda K H
0.311 0.129 0.373

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 3243

Number of extensions: 1668

Number of successful extensions: 10

Number of sequences better than 300.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 555

Length of database: 1,196,146,007

Length adjustment: 138

Effective length of query: 417

Effective length of database: 1,196,145,869

Effective search space: 498792827373

Effective search space used: 498792827373

Neighboring words threshold: 9

X1: 16 (7.2 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 42 (21.8 bits)

S2: 68 (30.8 bits)



Blast 2 Sequences results

PubMed

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BLAST

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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.13 [Nov-27-2005]

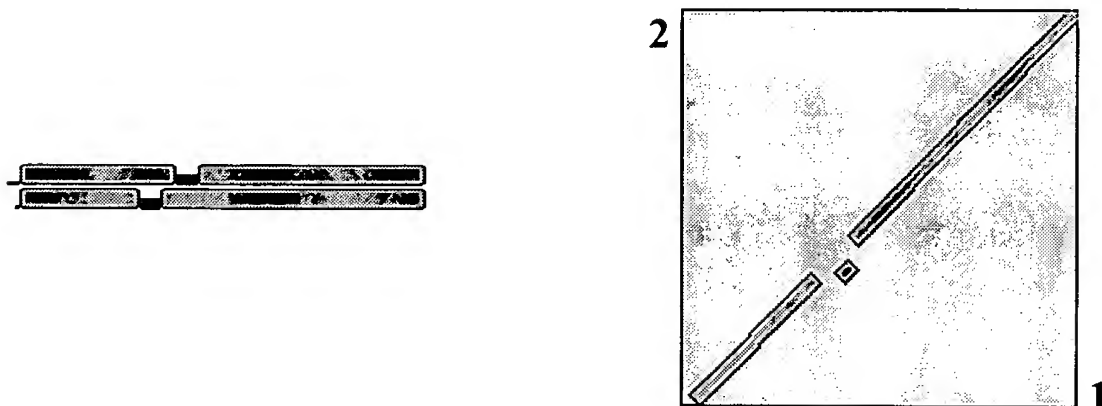
Matrix gap open: gap extension:
x_dropoff: expect: wordsize: Filter ☐ View option
Masking character option Masking color option
☐ Show CDS translation

Sequence 1: gi|1771282|emb|CAA69662.1|mDab555 protein [Mus musculus]

Length = 555 (1 .. 555)

Sequence 2: gi|76613795|ref|XP_582976.2|PREDICTED: similar to Disabled homolog 1 [Bos taurus]

Length = 542 (1 .. 542)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 938 bits (2424), Expect = 0.0

Identities = 480/567 (84%), Positives = 485/567 (85%), Gaps = 68/567 (11%)

Query	22	KGQDRSEATLIKRFKGEVRYKAKLIGIDEVSAARGDKLCQDSMMKLKGVVAGARSKGEH	81
		KGQDRSEATLIKRFKGEVRYKAKLIGIDEVSAARGDKLCQDSMMKLKGVVAGARSKGEH	
Sbjct	11	KGQDRSEATLIKRFKGEVRYKAKLIGIDEVSAARGDKLCQDSMMKLKGVVAGARSKGEH	70
Query	82	KQKIFLTISFGGIKIFDEKTGALQHHHAVHEISYIAKDITDHRAFGYVCGKEGNHRFVAI	141
		KQKIFLTISFGGIKIFDEKTGALQHHHAVHEISYIAKDITDHRAFGYVCGKEGNHRFVAI	
Sbjct	71	KQKIFLTISFGGIKIFDEKTGALQHHHAVHEISYIAKDITDHRAFGYVCGKEGNHRFVAI	130
Query	142	KTAQAAEPVILDLRDLFQLIYELKQREELEKKAQKDKQCEQAVYQTILEEDVEDPVYQYI	201
		KTAQAAEPVILDLRDLFQLIYELKQREELEKKAQKDKQCEQAVYQ	
Sbjct	131	KTAQAAEPVILDLRDLFQLIYELKQREELEKKAQKDKQCEQAVYQ-----	175
Query	202	VFEAGHEPIRDPETEENIYQVPTSQKKEGVYDVPKSQPV-----	241
		VPTSQKKEGVYDVPKSQPV	
Sbjct	176	-----VPTSQKKEGVYDVPKSQPVSNGRAFEDFDERFAAATPNRN	215
Query	242	-----AVTQLELFGDMSTPPDITSPPTPATPGDAFLPSSSQTLPGSADVFGS	288
		AVTQLELFGDMSTPPDITSPPTPATPGDAF+PSSSQTLPSADV GS	

Blast Result

Sbjct 216 LPMDFDEIFEATKAVTQLELFGDMSTPPDITSPPTPATPGDAFIPSSSQTLPASADVCGS 275

Query 289 MSFGTAAVPSGYVAMGAVLPSFWGQQPLVQQQIAMGAQPPVAQVIPGAQPIAWGQPGLEFP 348
+ FGTAAPVPSGYVAMGAVLPSFWGQQPLVQQQIAMGAQPPVAQV+PGAQPIAWGQPGLEFP

Sbjct 276 LPFGTAAVPSGYVAMGAVLPSFWGQQPLVQQQIAMGAQPPVAQVMPGAQPIAWGQPGLEFP 335

Query 349 ATQQAWPTVAGQFPFAAFMPTQTVMPLAAAMFQGPLTPLATVPGTND SARSSPQSDKPRQ 408
A QQ WP VAGQFPFAAFMPTQTVMPL AAMFQGPLTPLAT+P T DSARSSPQ+DKPRQ

Sbjct 336 AAQQPWPAVAGQFPFAAFMPTQTVMPLPAAMFQGPLTPLATIPATGDSARSSPQTDKPRQ 395

Query 409 KMGKESFKDFQM VQPPVPSRKPDQPSLTCTSEAFSSYFNKVGVAQDTDDCDDFDISQLN 468
KMGKE FKDFQM QPPVPSRKPDQPSLTCTSEAFSSYFNKVGVAQDTDDCDDFDISQLN

Sbjct 396 KMGKEMFKDFQMAQPPVPSRKPDQPSLTCTSEAFSSYFNKVGVAQDTDDCDDFDISQLN 455

Query 469 LTPVTSTTPSTNSPPTPAPRQSSPSKSSASHVSDPTADDIFEEGFESPSKSEEQEAPDGS 528
LTPVTSTTPSTNSPPTPAPRQSSPSKSSASH SDPTADDIFEEGFESPSKSEEQEAPDGS

Sbjct 456 LTPVTSTTPSTNSPPTPAPRQSSPSKSSASHASDPTADDIFEEGFESPSKSEEQEAPDGS 515

Query 529 QASSTSDPFGEPSEPSGDNISPQDGS 555
QASS SDPFGEPSEPSGDNISPQ GS

Sbjct 516 QASSNSDPFGEPSEPSGDNISPQAGS 542

1 - SEQ ID NO: 3 - 1

CPU time: 0.04 user secs. 0.01 sys. secs 0.05 total secs.

Lambda K H
0.311 0.129 0.373

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 3195

Number of extensions: 1648

Number of successful extensions: 13

Number of sequences better than 300.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 555

Length of database: 1,196,146,007

Length adjustment: 138

Effective length of query: 417

Effective length of database: 1,196,145,869

Effective search space: 498792827373

Effective search space used: 498792827373

Neighboring words threshold: 9

X1: 16 (7.2 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 42 (21.8 bits)

S2: 68 (30.8 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.13 [Nov-27-2005]

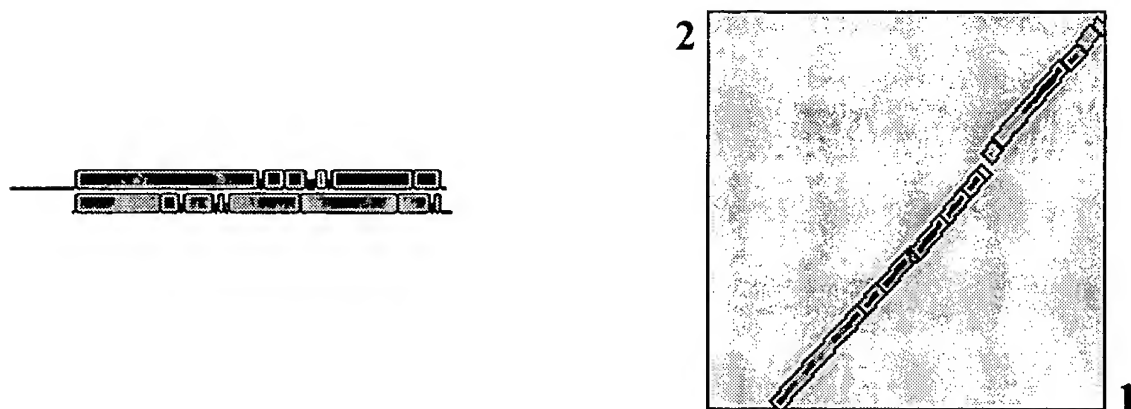
Matrix gap open: gap extension:
x_dropoff: expect: wordsize: Filter ☐ View option
Masking character option Masking color option
☐ Show CDS translation

Sequence 1: gi|1771282|emb|CAA69662.1|mDab555 protein [Mus musculus]

Length = 555 (1 .. 555)

Sequence 2: gi|68440873|ref|XP_686628.1|PREDICTED: similar to disabled homolog 1 [Danio rerio]

Length = 487 (1 .. 487)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.



Score = 585 bits (1509), Expect = 2e-165

Identities = 318/478 (66%), Positives = 359/478 (75%), Gaps = 34/478 (7%)

Query	97	FDEKTGALQHHAHVHEISYIAKDITDHRAFGYVCGKEGNHRFVAIKTAQAAEPVILDLRD	156
		F + LQHHAHVHEISYIAKDITDHRAFGYVCGKEGNHRFVAIKTAQ+AEPVILDLRD	
Sbjct	8	FRRDSEVLQHHAHVHEISYIAKDITDHRAFGYVCGKEGNHRFVAIKTAQSAEPVILDLRD	67
Query	157	LFQLIYELKQREELEKKAQKDKQCEQAVYQTILEEDVEDPVYQYIVFEAGHEPIRDPETE	216
		LFQLIYE+KQREE+EKKAQKDKQCEQAVYQTILEEDVEDPVYQYIVFEAGHEPIRDP +E	
Sbjct	68	LFQLIYEIKQREEIEKKAQKDKQCEQAVYQTILEEDVEDPVYQYIVFEAGHEPIRDP-SE	126
Query	217	ENIYQVPTSQKKEGVYDVPKSPVSAVTQLELFGDMSTPPDITSPPTPATPGDAFLPSSS	276
		E+IYQVPTSQ+KEGVYDVPK P + QLELFGDMSTPPDITSP TPA+P + P +	
Sbjct	127	ESIYQVPTSQQKEGVYDVPKRHP--NINQLELFGDMSTPPDITSPSTPASANTLDPLLA	184
Query	277	QTLPGSADVFGSMSFGTAAVPSGYVAMGAVLPSFWGQQPLVQQQIAMGAQPP--VAQVIP	334
		P +++F F A+VPSGYV MGAV P++ QQ Q +A G Q P VAQV+P	
Sbjct	185	HQTP--SELF--TPFNPAVPSGYVTMGAVPPAWAQQQFAAQAPLAFGVQSPVQAQVLP	240
Query	335	GAQPIAWGQPGLEPATQQAWPTVAG-QFPAAFMPTQTMPLAAAMFQGPLTPLA-----	388
		G QP+ WGQ LFPATQQ W +AG F PAAFMPTQTV PL AAMFQ L P+A	

Blast Result

Sbjct 241 GTQPLIWGQANLFPATQQQWAAMAGAHFSPAAFMPAQTVGPLPAAMFQ-TLAPMAVPASC 299

Query 389 -----TVFGTND SARSSPQSD-----KPRQKMGKESFKDFQMVQPPPVP SRKPDQPS 435
V GT+ S SSPQ + + KM KE FK+FQM +PP +P+RK +QPS

Sbjct 300 ETPTAAMGGAVAGTSASTASSPQH GERTLQRQAKMSKEMFKEFQMAKPPAMPARKGEQPS 359

Query 436 LTCTSEAFSSYFNKVGVAQDTDDCDDFDISQLNLTPVTSTTPSTNSPPTPAPRQSSPSKS 495
L+CT++AFSSYF++VG+AQDTDDCDDFDISQ+NLTPVTSTTPSTNSPPTPAPRQSSPSKS

Sbjct 360 LSCTTDAFSSYFSRVGMAQDTDDCDDFDISQMNLTPVTSTTPSTNSPPTPAPRQSSPSKS 419
1 - SEQ ID NO.3

Query 496 SASHVSDPTADDIFEEGFESPSKS-EEQEAPDGSQASSTSDPFGEPSGEP SGDNISPQ 552
SASH SDP DD F E SPS+S EE A D Q+ S+P EP S + SPQ

Sbjct 420 S-SHASDPPTDDSFGEAEGSPSRSGEEDAAGDCPQSPGASEPQAEPE---SSETDSPQ 473
-1

CPU time: 0.05 user secs. 0.01 sys. secs 0.06 total secs.

Lambda K H
0.311 0.129 0.373

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 2847

Number of extensions: 1507

Number of successful extensions: 18

Number of sequences better than 300.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 555

Length of database: 1,196,146,007

Length adjustment: 138

Effective length of query: 417

Effective length of database: 1,196,145,869

Effective search space: 498792827373

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